

10508.204-WO.ST25
SEQUENCE LISTING

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 <120> Protease Variants
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 <170> PatentIn version 3.2
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 <213> Nocardiopsis sp. NRRL 18262 ("Protease 10")

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<220>
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 ttctgcgacc gtcatgcgac ccatcatcggttgacccac cgagctctga atggtccacc 180
 gttctgacgg tctttccctc accaaaacgt gcacctatgg ttaggacgtt gtttaccgaa 240
 tgtctcggtg aacgacaggg gcccggacggattcggcccc gatccccctgt tgatcccccc 300
 aggagagtag ggaccccaatg cga ccc tcc ccc gtt gtc tcc gcc atc ggt 350
 Met Arg Pro Ser Pro Val Val Ser Ala Ile Gly
 -190 -185

acg gga gcg ctg gcc ttc ggt ctg gcg ctg tcc ggt acc ccg ggt 395
 Thr Gly Ala Leu Ala Phe Gly Leu Ala Leu Ser Gly Thr Pro Gly
 -180 -175 -170

gcc ctc gcg gcc acc gga gcg ctc ccc cag tca ccc acc ccg gag 440
 Ala Leu Ala Ala Thr Gly Ala Leu Pro Gln Ser Pro Thr Pro Glu
 -165 -160 -155

gcc gac gcg gtc tcc atg cag gag gcg ctc cag cgc gac ctc gac 485
 Ala Asp Ala Val Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Asp
 -150 -145 -140

ctg acc tcc gcc gag gcc gag gag ctg ctg gcc gcc cag gac acc 530
 Leu Thr Ser Ala Glu Ala Glu Glu Leu Leu Ala Ala Gln Asp Thr
 -135 -130 -125

gcc ttc gag gtc gac gag gcc gcg gcc gag gcc gac gac gcc 575
 Ala Phe Glu Val Asp Glu Ala Ala Ala Glu Ala Ala Gly Asp Ala
 -120 -115 -110

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 Tyr Gly Gly Ser Val Phe Asp Thr Glu Ser Leu Glu Leu Thr Val Leu
 -105 -100 -95

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gtc acc gat gcc gcc gtc gag gcc gtg gag gcc acc ggc gcc ggg Val Thr Asp Ala Ala Ala Val Glu Ala Val Glu Ala Thr Gly Ala Gly -90 -85 -80	671
acc gag ctg gtc tcc tac ggc atc gac ggt ctc gac gag atc gtc cag Thr Glu Leu Val Ser Tyr Gly Ile Asp Gly Leu Asp Glu Ile Val Gln -75 -70 -65	719
gag ctc aac gcc gcc gac gcc gtt ccc ggt gtg gtc ggc tgg tac ccg Glu Leu Asn Ala Ala Asp Ala Val Pro Gly Val Val Gly Trp Tyr Pro -60 -55 -50 -45	767
gac gtg gcg ggt gac acc gtc gtc ctg gag gtc ctg gag ggt tcc gga Asp Val Ala Gly Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly -40 -35 -30	815
gcc gac gtc agc ggc ctg ctc gcg gac gcc ggc gtg gac gcc tcg gcc Ala Asp Val Ser Gly Leu Leu Ala Asp Ala Gly Val Asp Ala Ser Ala -25 -20 -15	863
gtc gag gtg acc acg agc gac cag ccc gag ctc tac gcc gac atc atc Val Glu Val Thr Thr Ser Asp Gln Pro Glu Leu Tyr Ala Asp Ile Ile -10 -5 -1 1	911
ggt ggt ctg gcc tac acc atg ggc ggc cgc tgt tcg gtc ggc ttc gcg Gly Gly Leu Ala Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala 5 10 15 20	959
gcc acc aac gcc gcc ggt cag ccc ggg ttc gtc acc gcc ggt cac tgc Ala Thr Asn Ala Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys 25 30 35	1007
ggc cgc gtg ggc acc cag gtg acc atc ggc aac gac gcg gcc ttc gtc cgc ggt acg Gly Arg Val Gly Thr Gln Val Thr Ile Gly Asn Gly Arg Gly Val Phe 40 45 50	1055
gag cag tcc gtc ttc ccc ggc aac gac gcg gcc ttc gtc cgc ggt acg Glu Gln Ser Val Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr 55 60 65	1103
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tac gcc acg gtc gcc ggt cac aac cag gcc ccc atc ggc tcc tcc gtc Tyr Ala Thr Val Ala Gly His Asn Gln Ala Pro Ile Gly Ser Ser Val 85 90 95 100	1199
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cgc ggc cag tcg gtg agc tac ccc gag ggc acc gtc acc aac atg acc Arg Gly Gln Ser Val Ser Tyr Pro Glu Gly Thr Val Thr Asn Met Thr 120 125 130	1295
cgg acc acc gtg tgc gcc gag ccc ggc gac tcc ggc ggc tcc tac atc Arg Thr Thr Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile 135 140 145	1343
tcc ggc acc cag gcc cag ggc gtg acc tcc ggc ggc tcc ggc aac tgc Ser Gly Thr Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys 150 155 160	1391
cgc acc ggc ggg acc acc ttc tac cag gag gtc acc ccc atg gtg aac Arg Thr Gly Gly Thr Thr Phe Tyr Gln Glu Val Thr Pro Met Val Asn 165 170 175 180	1439

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tcc tgg ggc gtc cgt ctc cg acc tgatccccgc ggttccaggc ggaccgacgg 1493
 Ser Trp Gly Val Arg Leu Arg Thr
 185

tcgtgacctg agtaccaggc gtcccccggc cttccagcgg cgtccgcacc ggggtgggac 1553
 cggcggtggc cacggcccca cccgtgaccg gaccgcccgg cta 1596

<210> 2

<211> 382

<212> PRT

<213> Nocardiopsis sp. NRRL 18262 ("Protease 10")

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Ala Phe Gly Leu Ala Leu Ser Gly Thr Pro Gly Ala Leu Ala Ala
 -175 -170 -165

Thr Gly Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val
 -160 -155 -150

Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Asp Leu Thr Ser Ala
 -145 -140 -135

Glu Ala Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu Val
 -130 -125 -120

Asp Glu Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly Ser
 -115 -110 -105

Val Phe Asp Thr Glu Ser Leu Glu Leu Thr Val Leu Val Thr Asp Ala
 -100 -95 -90

Ala Ala Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Glu Leu Val
 -85 -80 -75

Ser Tyr Gly Ile Asp Gly Leu Asp Glu Ile Val Gln Glu Leu Asn Ala
 -70 -65 -60

Ala Asp Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala Gly
 -55 -50 -45

Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Ser
 -40 -35 -30 -25

Gly Leu Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val Thr
 -20 -15 -10

Thr Ser Asp Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu Ala
 -5 -1 1 5

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Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn Ala
 10 15 20

Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Arg Val Gly
 25 30 35 40

Thr Gln Val Thr Ile Gly Asn Gly Arg Gly Val Phe Glu Gln Ser Val
 45 50 55

Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe Thr
 60 65 70

Leu Thr Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr Ala Thr Val
 75 80 85

Ala Gly His Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser Gly
 90 95 100

Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln Ser
 105 110 115 120

Val Ser Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr Val
 125 130 135

Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Thr Gln
 140 145 150

Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly
 155 160 165

Thr Thr Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly Val
 170 175 180

Arg Leu Arg Thr
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<210> 3
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 <222> (1)..(1062)

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 -165 -160 -155 45

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gcc agc atg acc gag gcg ctc aag cgc gac ctc gac ctc acc tcg Ala Ser Met Thr Glu Ala Leu Lys Arg Asp Leu Asp Leu Thr Ser -150 -145 -140	90
gcc gag gcc gag gag ctt ctc tcg gcg cag gaa gcc gcc atc gag Ala Glu Ala Glu Glu Leu Leu Ser Ala Gln Glu Ala Ala Ile Glu -135 -130 -125	135
acc gac gcc gag gcc acc gag gcc gcg ggc gag gcc tac ggc ggc Thr Asp Ala Glu Ala Thr Glu Ala Ala Gly Glu Ala Tyr Gly Gly -120 -115 -110	180
tca ctg ttc gac acc gag acc ctc gaa ctc acc gtg ctg gtc acc gac Ser Leu Phe Asp Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp -105 -100 -95	228
gcc tcc gcc gtc gag gcg gtc gag gcc acc gga gcc cag gcc acc gtc Ala Ser Ala Val Glu Ala Val Glu Ala Thr Gly Ala Gln Ala Thr Val -90 -85 -80 -75	276
gtc tcc cac ggc acc gag ggc ctg acc gag gtc gtg gag gac ctc aac Val Ser His Gly Thr Glu Gly Leu Thr Glu Val Val Glu Asp Leu Asn -70 -65 -60	324
ggc gcc gag gtt ccc gag agc gtc ctc ggc tgg tac ccg gac gtg gag Gly Ala Glu Val Pro Glu Ser Val Leu Gly Trp Tyr Pro Asp Val Glu -55 -50 -45	372
agc gac acc gtc gtg gtc gag gtg ctg gag ggc tcc gac gcc gac gtc Ser Asp Thr Val Val Glu Val Leu Glu Gly Ser Asp Ala Asp Val -40 -35 -30	420
gcc gcc ctg ctc gcc gac gcc ggt gtg gac tcc tcc tcg gtc cggt gtg Ala Ala Leu Leu Ala Asp Ala Gly Val Asp Ser Ser Ser Val Val Arg Val -25 -20 -15	468
gag gag gcc gag gag gcc ccg cag gtc tac gcc gac atc atc atc ggc ggc Glu Glu Ala Glu Glu Ala Pro Gln Val Tyr Ala Asp Ile Ile Gly Gly -10 -5 -1 1 5	516
ctg gcc tac tac atg ggc ggc cgc tgc tcc gtc ggc ttc gcc gcg acc Leu Ala Tyr Tyr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr 10 15 20	564
aac agc gcc ggt cag ccc ggt ttc gtc acc gcc ggc cac tgc ggc acc Asn Ser Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Thr 25 30 35	612
gtc ggc acc ggc gtg acc atc ggc aac ggc acc ggc acc ttc cag aac Val Gly Thr Gly Val Thr Ile Gly Asn Gly Thr Gly Thr Phe Gln Asn 40 45 50	660
tcg gtc ttc ccc ggc aac gac gcc gcc ttc gtc cgc ggc acc tcc aac Ser Val Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn 55 60 65 70	708
ttc acc ctg acc aac ctg gtc tcg cgc tac aac tcc ggc ggc tac cag Phe Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Ser Gly Gly Tyr Gln 75 80 85	756
tcg gtg acc ggt acc agc cag gcc ccg gcc ggc tcg gcc gtg tgc cgc Ser Val Thr Gly Thr Ser Gln Ala Pro Ala Gly Ser Ala Val Cys Arg 90 95 100	804
tcc ggc tcc acc acc ggc tgg cac tgc ggc acc atc cag gcc cgc aac Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Asn 105 110 115	852

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cag acc gtg cgc tac ccg cag ggc acc gtc tac tcg ctc acc acc	900
Gln Thr Val Arg Tyr Pro Gln Gly Thr Val Tyr Ser Leu Thr Arg Thr	
120 125 130	
aac gtg tgc gcc gag ccc ggc gac tcc ggc ggt tcg ttc atc tcc ggc	948
Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser Gly	
135 140 145 150	
tcg cag gcc cag ggc gtc acc tcc ggc ggc tcc ggc aac tgc tcc gtc	996
Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Val	
155 160 165	
ggc ggc acg acc tac tac cag gag gtc acc ccg atg atc aac tcc tgg	1044
Gly Gly Thr Thr Tyr Tyr Gln Glu Val Thr Pro Met Ile Asn Ser Trp	
170 175 180	
ggt gtc agg atc cgg acc taa	1065
Gly Val Arg Ile Arg Thr	
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<211> 354

<212> PRT

<213> Nocardiopsis dassonvillei subspecies dassonvillei DSM 43235 ("Protease 18")

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Ala Ser Met Thr Glu Ala Leu Lys Arg Asp Leu Asp Leu Thr Ser
 -150 -145 -140

Ala Glu Ala Glu Glu Leu Leu Ser Ala Gln Glu Ala Ala Ile Glu
 -135 -130 -125

Thr Asp Ala Glu Ala Thr Glu Ala Ala Gly Glu Ala Tyr Gly Gly
 -120 -115 -110

Ser Leu Phe Asp Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp
 -105 -100 -95

Ala Ser Ala Val Glu Ala Val Glu Ala Thr Gly Ala Gln Ala Thr Val
 -90 -85 -80 -75

Val Ser His Gly Thr Glu Gly Leu Thr Glu Val Val Glu Asp Leu Asn
 -70 -65 -60

Gly Ala Glu Val Pro Glu Ser Val Leu Gly Trp Tyr Pro Asp Val Glu
 -55 -50 -45

Ser Asp Thr Val Val Val Glu Val Leu Glu Gly Ser Asp Ala Asp Val
 -40 -35 -30

Ala Ala Leu Leu Ala Asp Ala Gly Val Asp Ser Ser Ser Val Arg Val
 -25 -20 -15

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Glu Glu Ala Glu Glu Ala Pro Gln Val Tyr Ala Asp Ile Ile Gly Gly
-10 -5 -1 1 5

Leu Ala Tyr Tyr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr
10 15 20

Asn Ser Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Thr
25 30 35

Val Gly Thr Gly Val Thr Ile Gly Asn Gly Thr Gly Thr Phe Gln Asn
40 45 50

Ser Val Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn
55 60 65 70

Phe Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Ser Gly Gly Tyr Gln
75 80 85

Ser Val Thr Gly Thr Ser Gln Ala Pro Ala Gly Ser Ala Val Cys Arg
90 95 100

Ser Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Asn
105 110 115

Gln Thr Val Arg Tyr Pro Gln Gly Thr Val Tyr Ser Leu Thr Arg Thr
120 125 130

Asn Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Phe Ile Ser Gly
135 140 145 150

Ser Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Val
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Gly Val Arg Ile Arg Thr
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<210> 5
<211> 1062
<212> DNA
<213> Nocardiopsis prasina DSM 15648 ("Protease 11")

<220>
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<222> (1)..(1059)

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Val Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Gly Leu Thr Pro		
-150 -145 -140		
ctt gag gcc gat gaa ctg ctg gcc gcc cag gac acc gcc ttc gag		135
Leu Glu Ala Asp Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu		
-135 -130 -125		
gtc gac gag gcc gcg gcc gcg gcc gcc ggg gac gcc tac ggc ggc		180
Val Asp Glu Ala Ala Ala Ala Ala Gly Asp Ala Tyr Gly Gly		
-120 -115 -110		
tcc gtc ttc gac acc gag acc ctg gaa ctg acc gtc ctg gtc acc gac		228
Ser Val Phe Asp Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp		
-105 -100 -95 -90		
gcc gcc tcg gtc gag gct gtg gag gcc acc ggc gcg ggt acc gaa ctc		276
Ala Ala Ser Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Glu Leu		
-85 -80 -75		
gtc tcc tac ggc atc gag ggc ctc gac gag atc atc cag gat ctc aac		324
Val Ser Tyr Gly Ile Glu Gly Leu Asp Glu Ile Ile Gln Asp Leu Asn		
-70 -65 -60		
gcc gcc gac gcc gtc ccc ggc gtg gtc ggc tgg tac ccg gac gtg gcg		372
Ala Ala Asp Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala		
-55 -50 -45		
ggt gac acc gtc gtc ctg gag gtc ctg gag ggt tcc gga gcc gac gtg		420
Gly Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val		
-40 -35 -30 -25		
agc ggc ctg ctc gcc gac gcc ggc gtg gac gcc tcg gcc gtc gag gtg		468
Ser Gly Leu Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val		
-25 -20 -15 -10		
acc agc agt gcg cag ccc gag ctc tac gcc gac atc atc ggc ggt ctg		516
Thr Ser Ser Ala Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu		
-5 -1 1 5		
gcc tac acc atg ggc ggc cgc tgt tcg gtc gga ttc gcg gcc acc aac		564
Ala Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn		
10 15 20		
gcc gcc ggt cag ccc gga ttc gtc acc gcc ggt cac tgt ggc cgc gtg		612
Ala Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Arg Val		
25 30 35		
ggc acc cag gtg agc atc ggc aac ggc cag ggc gtc ttc gag cag tcc		660
Gly Thr Gln Val Ser Ile Gly Asn Gly Gln Gly Val Phe Glu Gln Ser		
40 45 50 55		
atc ttc ccg ggc aac gac gcc gcc ttc gtc cgc ggc acg tcc aac ttc		708
Ile Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe		
60 65 70		
acg ctg acc aac ctg gtc agc cgc tac aac acc ggc ggt tac gcc acc		756
Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr Ala Thr		
75 80 85		
gtc gcc ggc cac aac cag gcg ccc atc ggc tcc tcc gtc tgc cgc tcc		804
Val Ala Gly His Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser		
90 95 100		

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ggc tcc acc acc ggc tgg cac tgc ggc acc atc cag gcc cgc ggc cag Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln 105 110 115	852
tcg gtg agc tac ccc gag ggc acc gtc acc aac atg acc cg ^g acc acc Ser Val Ser Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr 120 125 130 135	900
gtg tgc gcc gag ccc ggc gac tcc ggc ggc tcc tac atc tcc ggc aac Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Asn 140 145 150	948
cag gcc cag ggc gtc acc tcc ggc ggc tcc ggc aac tgc cgc acc ggc Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly 155 160 165	996
ggg acc acc ttc tac cag gag gtc acc ccc atg gtg aac tcc tgg ggc Gly Thr Thr Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly 170 175 180	1044
gtc cgt ctc cgg acc taa Val Arg Leu Arg Thr 185	1062

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<211> 353

<212> PRT

<213> Nocardiopsis prasina DSM 15648 ("Protease 11")

<400> 6

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Val Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Gly Leu Thr Pro -150 -145 -140

Leu Glu Ala Asp Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu -135 -130 -125

Val Asp Glu Ala Ala Ala Ala Ala Ala Gly Asp Ala Tyr Gly Gly -120 -115 -110

Ser Val Phe Asp Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp -105 -100 -95 -90
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Ala Ala Ser Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Glu Leu -85 -80 -75
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Val Ser Tyr Gly Ile Glu Gly Leu Asp Glu Ile Ile Gln Asp Leu Asn -70 -65 -60
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Ala Ala Asp Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala -55 -50 -45
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Gly Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val -40 -35 -30
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Ser Gly Leu Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val
 -25 -20 -15 -10

Thr Ser Ser Ala Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu
 -5 -1 1 5

Ala Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn
 10 15 20

Ala Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Arg Val
 25 30 35

Gly Thr Gln Val Ser Ile Gly Asn Gly Gln Gly Val Phe Glu Gln Ser
 40 45 50 55

Ile Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe
 60 65 70

Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr Ala Thr
 75 80 85

Val Ala Gly His Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser
 90 95 100

Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln
 105 110 115

Ser Val Ser Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr
 120 125 130 135

Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Asn
 140 145 150

Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly
 155 160 165

Gly Thr Thr Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly
 170 175 180

Val Arg Leu Arg Thr
 185

<210> 7

<211> 1062

<212> DNA

<213> Nocardiopsis prasina DSM 15649 ("Protease 35")

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<222> (1)..(1059)

<220>

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<221> mat_peptide
<222> (496)..(1059)

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90 95 100	
ggc tcc acc acc ggt tgg cac tgc ggc acc atc cag gcc cgc ggc cag Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln	852
105 110 115	
tcg gtg agc tac ccc gag ggc acc gtc acc aac atg acg cgg acc acc Ser Val Ser Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr	900
120 125 130 135	
gtg tgc gcc gag ccc ggc gac tcc ggc tcc tac atc tcc ggc aac Val Cys Ala Glu Pro Gly Asp Ser Gly Ser Tyr Ile Ser Gly Asn	948
140 145 150	
cag gcc cag ggc gtc acc tcc ggc ggc tcc ggc aac tgc cgc acc ggc Gln Ala Gln Gly Val Thr Ser Gly Ser Gly Asn Cys Arg Thr Gly	996
155 160 165	
ggg acc acc ttc tac cag gag gtc acc ccc atg gtg aac tcc tgg ggc Gly Thr Thr Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly	1044
170 175 180	
gtc cgt ctc cgg acc taa Val Arg Leu Arg Thr	1062
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<212> PRT

<213> Nocardiopsis prasina DSM 15649 ("Protease 35")

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Val Ser Met Gln Glu Ala Leu Gln Arg Asp Leu Gly Leu Thr Pro
-150 -145 -140

Leu Glu Ala Asp Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu
-135 -130 -125

Val Asp Glu Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly
-120 -115 -110

Ser Val Phe Asp Thr Glu Thr Leu Glu Leu Thr Val Leu Val Thr Asp
-105 -100 -95 -90

Ser Ala Ala Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Glu Leu
-85 -80 -75

Val Ser Tyr Gly Ile Thr Gly Leu Asp Glu Ile Val Glu Glu Leu Asn
-70 -65 -60

Ala Ala Asp Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala
-55 -50 -45

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Gly Asp Thr Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val
-40 -35 -30

Gly Gly Leu Leu Ala Asp Ala Gly val Asp Ala ser Ala val Glu val
-25 -20 -15 -10

Thr Thr Thr Glu Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu
-5 -1 1 5

Ala Tyr Thr Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn
10 15 20

Ala Ala Gly Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Arg Val
25 30 35

Gly Thr Gln Val Thr Ile Gly Asn Gly Arg Gly Val Phe Glu Gln Ser
40 45 50 55

Ile Phe Pro Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe
60 65 70

Thr Leu Thr Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr Ala Thr
75 80 85

Val Ala Gly His Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser
90 95 100

Gly Ser Thr Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln
105 110 115

Ser Val Ser Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr
120 125 130 135

Val Cys Ala Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Asn
140 145 150

Gln Ala Gln Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly
155 160 165

Gly Thr Thr Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly
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Val Arg Leu Arg Thr
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<210> 9
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<213> Nocardiopsis alba DSM 15647 ("Protease 08")

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<220>

<221> mat_peptide

<222> (502)..(1065)

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-165 -160 -155	

gcc acc acc atg gtc gag gcc ctc cag cgc gac ctc ggc ctg tcc	90
Ala Thr Thr Met Val Glu Ala Leu Gln Arg Asp Leu Gly Leu Ser	
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gtcgacgcgg cggttcgcgt ccggacagca catcacccgaa atattatggaa agaaaatatc agcaccatga cggccaaacg gatgcttcca acggtgctaa ctatatcact atgtcctaca actattatca cgatcatgat aaaagctcca ttttcggatc aagtgcacgc aaaacctccg atgacggcaa attaaaaatt acgctgcac tcataccgcta taaaaatatt gtccagcgcg cgccgagagt ccgcttcggg caagtgcacg tatacaacaa ctattatgaa ggaaggacacaa gctcttcaag ttatcctttt agctatgcat gggaaatcg aaagtcatct aaaatctatg ccccaaaacaa tgtcattgac gtaccggac tgtcagctgc taaaacgatc agcgtattca gcggggaaac ggctttat gactccggca cgttgctgaa cgccacacacatcaacgcac cggtgcacaa cgggctgagc tcttctgtcg gctggacgcc gtctctgcatttggatcatttca atgcttctgc taatgtgaaa tcaaatttta taaatcaacg gggtgccgggt aaattaaatt aagaaagtga aaaacacaaa gggtgctaac ctttggatc tttaattttt taaaatgttt atataacttag ttaaggagta gaatggaaaa gggatcgaa aaacaagtat ataggaggag acctatttat ggcttcagaa aaagacgcac gaaaacagtc agcagtaaag cttgttccat tgcttattac tgctgtgtg ggactaatca tctggtttat tcccgctccg tccggacttg aacctaaac ttggcattttt tttgcatttt ttgtcgcaac aattatcgcc tttatctcca agcccttgcc aatgggtgca attgcaattt ttgcattggc ggttactgca ctaactggaa cactatcaat tgaggataca ttaagcgat tcggaaataa gaccattgg cttatcgta tcgcattttt tatttcccgg ggatttatca aaaccggctc cggtgccgaga atttcgtatg tattcgttca gaaattcgga aaaaaaacc ttggactttc ttattcactg ctattcgtatg atataactttt ttcacactgct attccaagta atacggcgcc tgcaggaggc attatatttc ctattatcg atcattatcc gaaacattcg gatcaagccc ggcaaatggaa acagagagaa aaatcggtgc attcttatta aaaaccggtt ttcaaggaa tctgatcaca tctgctatgt tcctgacagc gatggcggcg aacccgctga ttgccaagct ggcccatgat gtcgcagggg tggacttaac atggacaagc tggcaattt ccgcgattgt accgggactt gtaagcttaa tcatcacgcc gcttgtgatt tacaaactgt atccgcccga aatcaaagaa acaccggatg cgcgaaaaat cgcaacagaa aaactgaaag aaatgggacc gttcaaaaaa tcggagctt 8387	6887 6947 7007 7067 7127 7187 7247 7307 7367 7427 7487 7547 7607 7667 7727 7787 7847 7907 7967 8027 8087 8147 8207 8267 8327

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ccatggttat cgtgtttctt ttgggtgcttg tgctgtggat tttggcggc agttcaaca	8447
tcgacgctac cacaaccgca ttgatcggtt tggccgttct cttattatca caagttctga	8507
cttggatga tatcaagaaa gaacaggcg cttggatac gctcaactgg tttgcggcgc	8567
ttgtcatgct cgccaacttc ttgaatgaat taggcatggt gtcttggttc agtaatgcc	8627
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attattactc tcactatttc tttgcaagtg cgacagccca catcagtgcg atgtattcag	8747
cattttggc tgtcgctgt gcagcggcg caccgccct ttttagcagcg ctgagcctcg	8807
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tgagtgtgat tgctgtgctt gtactgctgc tcggattat tggcgccgcgt gtgctggcga	9707
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aatgctgcc gaaccaggaa gtaagcgtca acgatcaagt gtttattatc aatacgaaag	10007
tgatgaatca aggccccag gcgtatggc ttgtcgatcg cttcaggagaaaacagagc	10067
tgaagaagct gatcgacaca ttgacagagg ttgcacaaata ttcagaggat ctcaggcgc	10127
aqactcatqa atttcaaata aagctttatg cgattttagg gctgc	10172

<210> 14
<211> 380
<212> PRT
<213> Artificial

<220>
<223> synthetic Construct

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<400> 14

Met Lys Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu
 -190 -185 -180
 Ile Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Thr Gly
 -175 -170 -165
 Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val Ser Met
 -160 -155 -150
 Gln Glu Ala Leu Gln Arg Asp Leu Asp Leu Thr Ser Ala Glu Ala
 -145 -140 -135
 Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu Val Asp Glu
 -130 -125 -120
 Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly Ser Val Phe
 -115 -110 -105
 Asp Thr Glu Ser Leu Glu Leu Thr Val Leu Val Thr Asp Ala Ala Ala
 -100 -95 -90
 Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Glu Leu Val Ser Tyr
 -85 -80 -75
 Gly Ile Asp Gly Leu Asp Glu Ile Val Gln Glu Leu Asn Ala Ala Asp
 -70 -65 -60 -55
 Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala Gly Asp Thr
 -50 -45 -40
 Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Ser Gly Leu
 -35 -30 -25
 Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val Thr Thr Ser
 -20 -15 -10
 Asp Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu Ala Tyr Thr
 -5 -1 1 5 10
 Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn Ala Ala Gly
 15 20 25
 Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Arg Val Gly Thr Gln
 30 35 40
 Val Thr Ile Gly Asn Gly Arg Gly Val Phe Glu Gln Ser Val Phe Pro
 45 50 55
 Gly Asn Asp Ala Ala Phe Val Arg Gly Thr Ser Asn Phe Thr Leu Thr

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60	65	70																																										
Asn Leu Val Ser Arg Tyr Asn Thr Gly Gly Tyr Ala Thr Val Ala Gly																																												
75	80	85	90			His Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser Gly Ser Thr			95	100	105	Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln Ser Val Ser			110	115	120	Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr Val Cys Ala			125	130	135	Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Thr Gln Ala Gln			140	145	150	Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr			155	160	165	170			Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly Val Arg Leu			175	180	185
90																																												
His Asn Gln Ala Pro Ile Gly Ser Ser Val Cys Arg Ser Gly Ser Thr																																												
95	100	105																																										
Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Gly Gln Ser Val Ser																																												
110	115	120																																										
Tyr Pro Glu Gly Thr Val Thr Asn Met Thr Arg Thr Thr Val Cys Ala																																												
125	130	135																																										
Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Thr Gln Ala Gln																																												
140	145	150																																										
Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Arg Thr Gly Gly Thr Thr																																												
155	160	165	170			Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly Val Arg Leu			175	180	185																																	
170																																												
Phe Tyr Gln Glu Val Thr Pro Met Val Asn Ser Trp Gly Val Arg Leu																																												
175	180	185																																										

Arg Thr

<210> 15
<211> 35
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 15
ggagctctga aaaaaaggag aggataaaga atgaa

35

<210> 16
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 16
gcgttccgat aatcgcggtg acaatgccg

29

<210> 17
<211> 29
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 17

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29

ttcatgagtc tgccctgt gatcctctg

<210> 18
<211> 30
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 18
taatcgcatg ttcaatccgc tccataatcg

30

<210> 19
<211> 44
<212> DNA
<213> Artificial

<220>
<223> Primer

<400> 19
cccaacggtt tcttcattct ttatcctctc cttttttca gagc

44

<210> 20
<211> 1164
<212> DNA
<213> Artificial

<220>
<223> Protease 22

<220>
<221> CDS
<222> (1)..(1164)

<220>
<221> sig_peptide
<222> (1)..(81)

<220>
<221> mat_peptide
<222> (577)..(1164)

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att tca gtg gca ttt agc tca tct att gca tca gca gct aca gga Ile Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Thr Gly -175 -170 -165	90
gca tta ccg cag tct ccg aca ccg gaa gca gat gca gtc tca atg Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val Ser Met -160 -155 -150	135
caa gaa gca ctg caa aga gat ctt gat ctt aca tca gca gaa gca Gln Glu Ala Leu Gln Arg Asp Leu Asp Leu Thr Ser Ala Glu Ala -145 -140 -135	180
gaa gaa ctt ctt gct gca caa gat aca gca ttt gaa gtg gat gaa Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu Val Asp Glu -130 -125 -120	225

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gca gcg gca gaa gca gca gga gat gca tat ggc ggc tca gtt ttt Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly Ser Val Phe -115 -110 -105	270
gat aca gaa tca ctt gaa ctt aca gtt ctt gtt aca gat gca gca gca Asp Thr Glu Ser Leu Glu Leu Thr Val Leu Val Thr Asp Ala Ala Ala -100 -95 -90	318
gtt gaa gca gtt gaa gca aca gga gca gga aca gta ctt gtt tca tat Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Val Leu Val Ser Tyr -85 -80 -75	366
gga att gat ggc ctt gat gaa att gtt caa gaa ctg aat gca gct gat Gly Ile Asp Gly Leu Asp Glu Ile Val Gln Glu Leu Asn Ala Ala Asp -70 -65 -60 -55	414
gct gtt ccg ggc gtt gtt ggc tgg tat ccg gat gtt gct gga gat aca Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala Gly Asp Thr -50 -45 -40	462
gtt gtc ctt gaa gtt ctt gaa gga tca ggc gca gat gtt tca ggc ctg Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Ser Gly Leu -35 -30 -25	510
ctg gca gac gca gga gtc gat gca tca gca gtt gaa gtt aca aca tca Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val Thr Thr Ser -20 -15 -10	558
gat caa ccg gaa ctt tat gca gat att att ggc ggc ctg gca tat tat Asp Glu Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu Ala Tyr Tyr -5 -1 1 5 10	606
atg ggc ggc aga tgc agc gtt ggc ttt gca gca aca aat gca tca ggc Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn Ala Ser Gly 15 20 25	654
caa ccg ggc ttt gtt aca gca ggc cat tgc ggc aca gtt ggc aca cca Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Thr Val Gly Thr Pro 30 35 40	702
gtt tca att ggc aat ggc aaa ggc gtt ttt gaa cga agc att ttt ccg Val Ser Ile Gly Asn Gly Lys Gly Val Phe Glu Arg Ser Ile Phe Pro 45 50 55	750
ggc aat gat tca gca ttt gtt aga ggc aca tca aat ttt aca ctt aca Gly Asn Asp Ser Ala Phe Val Arg Gly Thr Ser Asn Phe Thr Leu Thr 60 65 70	798
aat ctg gtt tca aga tat aat tca ggc ggc tat gca aca gtt gca ggc Asn Leu Val Ser Arg Tyr Asn Ser Gly Gly Tyr Ala Thr Val Ala Gly 75 80 85 90	846
cat aat caa gca ccg att ggc tca gca gtt tgc aga tca ggc tca aca His Asn Gln Ala Pro Ile Gly Ser Ala Val Cys Arg Ser Gly Ser Thr 95 100 105	894
aca ggc tgg cat tgc ggc aca att caa gca aga aat caa aca gtt agg Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Asn Gln Thr Val Arg 110 115 120	942
tat ccg caa ggc aca gtt tat agt ctg aca aga aca aca gtt tgt gca Tyr Pro Gln Gly Thr Val Tyr Ser Leu Thr Arg Thr Thr Val Cys Ala 125 130 135	990
gaa ccg ggc gat tca ggc ggc tca tat att agc ggc act caa gca caa Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Thr Gln Ala Gln 140 145 150	1038

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ggc gtt aca tca ggc ggc tca ggc aat tgc agt gct ggc ggc aca aca	1086
Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Ala Gly Gly Thr Thr	
155 160 165 170	
tat tac caa gaa gtt aat ccg atg ctt agt tca tgg ggc ctt aca ctt	1134
Tyr Tyr Gln Glu Val Asn Pro Met Leu Ser Ser Trp Gly Leu Thr Leu	
175 180 185	
aga aca caa tcg cat gtt caa tcc gct cca	1164
Arg Thr Gln Ser His Val Gln Ser Ala Pro	
190 195	

<210> 21
<211> 388
<212> PRT
<213> Artificial

<220>
<223> Synthetic Construct

<400> 21

Met Lys Lys Pro Leu Gly Lys Ile Val Ala Ser Thr Ala Leu Leu
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Ile Ser Val Ala Phe Ser Ser Ser Ile Ala Ser Ala Ala Thr Gly
-175 -170 -165

Ala Leu Pro Gln Ser Pro Thr Pro Glu Ala Asp Ala Val Ser Met
-160 -155 -150

Gln Glu Ala Leu Gln Arg Asp Leu Asp Leu Thr Ser Ala Glu Ala
-145 -140 -135

Glu Glu Leu Leu Ala Ala Gln Asp Thr Ala Phe Glu Val Asp Glu
-130 -125 -120

Ala Ala Ala Glu Ala Ala Gly Asp Ala Tyr Gly Gly Ser Val Phe
-115 -110 -105

Asp Thr Glu Ser Leu Glu Leu Thr Val Leu Val Thr Asp Ala Ala Ala
-100 -95 -90

Val Glu Ala Val Glu Ala Thr Gly Ala Gly Thr Val Leu Val Ser Tyr
-85 -80 -75

Gly Ile Asp Gly Leu Asp Glu Ile Val Gln Glu Leu Asn Ala Ala Asp
-70 -65 -60 -55

Ala Val Pro Gly Val Val Gly Trp Tyr Pro Asp Val Ala Gly Asp Thr
-50 -45 -40

Val Val Leu Glu Val Leu Glu Gly Ser Gly Ala Asp Val Ser Gly Leu
-35 -30 -25

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Leu Ala Asp Ala Gly Val Asp Ala Ser Ala Val Glu Val Thr Thr Ser
-20 -15 -10

Asp Gln Pro Glu Leu Tyr Ala Asp Ile Ile Gly Gly Leu Ala Tyr Tyr
-5 -1 1 5 10

Met Gly Gly Arg Cys Ser Val Gly Phe Ala Ala Thr Asn Ala Ser Gly
15 20 25

Gln Pro Gly Phe Val Thr Ala Gly His Cys Gly Thr Val Gly Thr Pro
30 35 40

Val Ser Ile Gly Asn Gly Lys Gly Val Phe Glu Arg Ser Ile Phe Pro
45 50 55

Gly Asn Asp Ser Ala Phe Val Arg Gly Thr Ser Asn Phe Thr Leu Thr
60 65 70

Asn Leu Val Ser Arg Tyr Asn Ser Gly Gly Tyr Ala Thr Val Ala Gly
75 80 85 90

His Asn Gln Ala Pro Ile Gly Ser Ala Val Cys Arg Ser Gly Ser Thr
95 100 105

Thr Gly Trp His Cys Gly Thr Ile Gln Ala Arg Asn Gln Thr Val Arg
110 115 120

Tyr Pro Gln Gly Thr Val Tyr Ser Leu Thr Arg Thr Thr Val Cys Ala
125 130 135

Glu Pro Gly Asp Ser Gly Gly Ser Tyr Ile Ser Gly Thr Gln Ala Gln
140 145 150

Gly Val Thr Ser Gly Gly Ser Gly Asn Cys Ser Ala Gly Gly Thr Thr
155 160 165 170

Tyr Tyr Gln Glu Val Asn Pro Met Leu Ser Ser Trp Gly Leu Thr Leu
175 180 185

Arg Thr Gln Ser His Val Gln Ser Ala Pro
190 195